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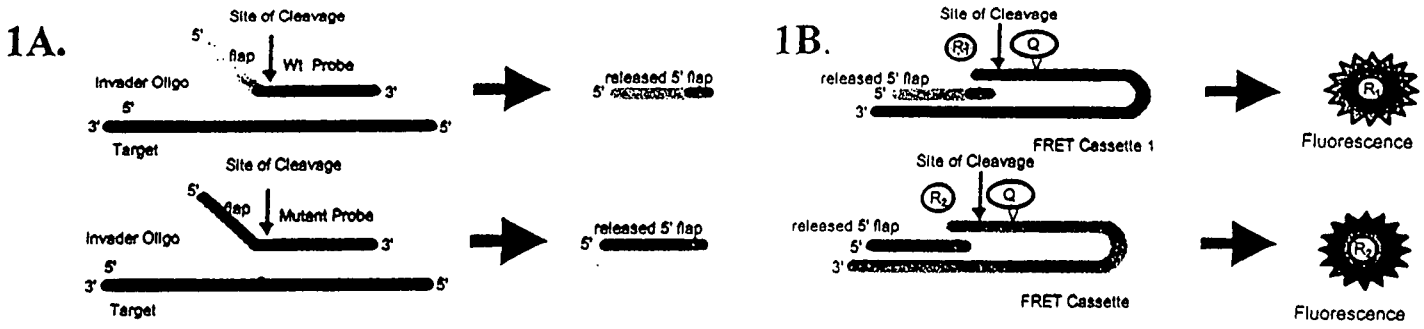
# FIGURE 1




"Replacement Sheet"

# FIGURE 2

# Automated primer selection for multiplex PCR using *Invader™ Creator Primer Designer v 1.3.3*

Multiplex PCR commonly requires extensive optimization to avoid biased amplification of select amplicons and the amplification of spurious products resulting from the formation of primer-dimers. In order to avoid these problems, we have designed *Invader™ Creator Primer Designer v1.3.3* software for the automated selection of multiplex primers. Beginning with a set of user defined sequences and corresponding SNP locations, *Invader ™ Creator Primer Designer* defines an "Invader™ footprint" (the minimal amplicon required for Invader™ detection) for each sequence. Primers are designed outward from the "Invader™ footprint" and evaluated against several criteria, including the potential for primer-dimer formation with previously designed primers in the current multiplexing set. *Invader ™ Creator Primer Designer* continues through multiple iterations of the same set of sequences until primers against all sequences in the current multiplexing set can be designed.

## 2A. (SEQ ID NO:263)

```
29043,FMO1,aagttagaagaaccaagactatcttgtcaggggtgtattttgagagtggcagacttttcagtgcct
ttccattcatgacacttcttgaatctctggcagaaccagccagccgtgttcacagtgtcaaatgaagggatgtcttt
gattgcttccaggtgttcctcagcaccaccggaggggggatgggtgatcagccgaatctttgactcgggctacccatg
ggacatggtgttcatgacacgctttcagaacatgttgagaaattccctcccaac[ct]ccaattgtgacttggttga
tggagcgaaagataaacaactggctcaatcatgcaaattacggcttaataccagaagacaggtaaatataatgtgac
tgccaagggcttttaggaagaaggagcctctgcctgtccagcagcctatacaagccaggcagtaccacagcaacatg
gctgaatgtgtgggaacacttgatacaaatttgcttgataataacagctaactgttcttaagtactcagaaagtgaa
attatgtatttc
```

## 2B. (SEQ ID NO:263)

```
29043,FMO1,aagttagaagaaccaagactatcttgtcaggggtgtattttgagagtggcagacttttcagtgcct
ttccattcatgacacttcttgaatctctggcagaaccagccagccgtgttcacagtgtcaaatgaagggatgtcttt
gattgcttccaggtgttcctcagcaccaccggaggggggatgggtgatcagccgaatctttgactcgggctacccatg
ggacatggtgttCATGACACGCTTTCAGAACATGTTGAGAAATTCCCTCCCAAC[ct]CCAATTGTGACTTGGTTGA
TGGAGCGAAAGATAAACAACTGGctcaatcatgcaaattacggcttaataccagaagacaggtaaatataatgtgac
tgccaagggcttttaggaagaaggagcctctgcctgtccagcagcctatacaagccaggcagtaccacagcaacatg
gctgaatgtgtgggaacacttgatacaaatttgcttgataataacagctaactgttcttaagtactcagaaagtgaa
attatgtatttc

f,cgggctacccatgggaca,59.38 (SEQ ID NO:333)
r,tctggtattaagccgtaatttgcatgattga,60 (SEQ ID NO:334)
```

**Figure 2. Creation of 101 primer sets from sequences available for analysis on the Invader™ *M*edically *A*ssociated *P*anel using Invader ™ Creator Primer Designer v 1.3.3.** (A) Sample input file of a single entry. Information includes TWT SNP#, short name identifier, and sequence with the SNP location indicated in brackets. (B) Sample output file of the same entry. Information includes the sequence of the "Invader footprint" (capital letters flanking SNP site), forward and reverse primer sequences (bold), and their corresponding Tm's.

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# Figure 5A

CYP2D6 PCR amplification:

Primers:

Triplex PCR protocol

Exons 1 & 2 (2036 nt)

2D6L1F1: 5' – CTGGGCTGGGAGCAGCCTC - 3' (SEQ ID NO:335)
2D6L1R1: 5' – CACTCGCTGGCCTGTTTCATGTC – 3' (SEQ ID NO:336)

Exons 3, 4, 5, & 6 (1683 nt)

2D6L2F: 5' – CTGGAATCCGGTGTCGAAGTGG – 3' (SEQ ID NO:337)
2D6L2R2: 5' – CTCGGCCCCTGCACTGTTTC – 3' (SEQ ID NO:338)

Exons 7, 8, & 9 (1754 nt)

2D6L3F: 5' – GAGGCAAGAAGGAGTGTCAGGG – 3' (SEQ ID NO:339)
2D6L3R5B: 5' – AGTCCTGTGGTGAGGTGACGAGG – 3' (SEQ ID NO:340)

Monoplex PCR protocol

CYP2D6 nucleotides 506 – 856 (*10 & *21)

forward (1221-09-01): 5' – ggtagtgaggcaggt –3' (SEQ ID NO:341)
reverse (1221-09-02): 5' – gcttctggtaggggag – 3' (SEQ ID NO:342)

CYP2D6 nucleotides 1335 – 1616 (*11 & *17)

forward (1221-09-03): 5' – aaataggactaggacctgt –3' (SEQ ID NO:343)
reverse (1221-09-04): 5' – gggtcccacggaaat – 3' (SEQ ID NO:344)

CYP2D6 nucleotides 2092 – 2582 (*4, *6 & *37)

forward (1221-09-05): 5' – catggccacgcg –3' (SEQ ID NO:345)
reverse (1221-09-06): 5' – ccggcacctctcg – 3' (SEQ ID NO:346)

CYP2D6 nucleotides 2977 – 3146 (*3 & *33)

forward (1221-09-07): 5' – ccgtcctcctgcat –3' (SEQ ID NO:347)
reverse (1221-09-08): 5' – cactctcaccttctcca – 3' (SEQ ID NO:348)

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# Figure 5B

CYP2D6 nucleotides 3294 – 3494 (*2 R296C & *7)

forward (1221-09-09): 5' – gttctgtcccgagtatg –3' (SEQ ID NO:349)
reverse (1221-09-10): 5' – tgcactgtttcccaga – 3' (SEQ ID NO:350)

CYP2D6 nucleotides 3589 – 3918 (*25, *26 & *29)

forward (1221-09-11): 5' – ctgacctcctccaacat –3' (SEQ ID NO:351)
reverse (1221-09-12): 5' – gggctatcaccaggt – 3' (SEQ ID NO:352)

CYP2D6 nucleotides 4316 – 5226 (*2, *27, *31 & *32)

forward (1221-09-13): 5' – ctgacctcctccaacat –3' (SEQ ID NO:353)
reverse (1221-09-15): 5' – gggctatcaccaggt – 3' (SEQ ID NO:354)

# FIGURE 14

| Primer Name | Sequence | Size | Oligo TM | Amplicon Size |
|---|---|---|---|---|
| primer pair 1 | AAG GCT TTG CAG GCT TCA (SEQ ID NO:355) | 18 bases | 64.3 | |
| primer pair 1 | GCT CGG ACT ACG GTC ATC A (SEQ ID NO:356) | 19 bases | 65.3 | 1460 bp |
| | | | | |
| primer pair 2 | TGG AAT CCG GTG TCG AAG (SEQ ID NO:357) | 18 bases | 63.4 | |
| primer pair 2 | GAA ATC TCT GAC GTG GAT AG (SEQ ID NO:358) | 20 bases | 58.8 | 942 bp |
| | | | | |
| primer pair 3 | GTA CCT CCT ATC CAC GTC A (SEQ ID NO:359) | 19 bases | 61.7 | |
| primer pair 3 | CAC TCC TTC TTG CCT CCT A (SEQ ID NO:360) | 19 bases | 62.2 | 866 bp |
| | | | | |
| primer pair 4 | GCA AGA AGG AGT GTC AGG G (SEQ ID NO:361) | 19 bases | 64.1 | |
| primer pair 4 | CTG TGG TGA GGT GAC GAG G (SEQ ID NO:362) | 19 bases | 66.1 | 1748 bp |

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**FIGURE 15**

| SNP Name | Nucleotide position/ change | Oligo Type | Dye | Poly-morphism | Assay Oligo Sequence |
|---|---|---|---|---|---|
| CYP2D6 S486T | 4180G>C | Invader | NONE | | GCCACCATGGTGTCTTTGCTTTCCTGGTGAT (SEQ ID NO:363) |
| CYP2D6 S486T | 4180G>C | Probe | FAM | C | CGCGCCGAGGCCCCATCCCCCTATGV (SEQ ID NO:364) |
| CYP2D6 S486T | 4180G>C | Probe | RED | G | ACGGACGCGGAGGCCCATCCCCCTATV (SEQ ID NO:365) |
| CYP2D6 S486T | 4180G>C | Target | FAM | C | AGCTCATAGGGGGATGGGGTCACCAGGAAAGCAAAGACACCATGGTGGCTG (SEQ ID NO:366) |
| CYP2D6 S486T | 4180G>C | Target | RED | G | AGCTCATAGGGGGATGGGCTCACCAGGAAAGCAAAGACACCATGGTGGCTG (SEQ ID NO:367) |
| | | | | | |
| CYP2D6 1846G>A | 1846G>A | Invader | NONE | | CCTTACCCGCATCTCCCACCCCCAT (SEQ ID NO:368) |
| CYP2D6 1846G>A | 1846G>A | Probe | FAM | A | CGCGCCGAGGAGACGCCCCTTTCGV (SEQ ID NO:369) |
| CYP2D6 1846G>A | 1846G>A | Probe | RED | G | ACGGACGCGGAGGGACGCCCCTTTCV (SEQ ID NO:370) |
| CYP2D6 1846G>A | 1846G>A | Target | FAM | A | GGGGCGAAAGGGGCGTCTTGGGGGTGGGAGATGCGGGTAAGGGG (SEQ ID NO:371) |
| CYP2D6 1846G>A | 1846G>A | Target | RED | G | GGGGCGAAAGGGGCGTCCTGGGGGTGGGAGATGCGGGTAAGGGG (SEQ ID NO:372) |
| | | | | | |
| CYP2D6 H324P | 2935A>C | Invader | NONE | | GGGCTCACGCTGCACATCCGGAC (SEQ ID NO:373) |
| CYP2D6 H324P | 2935A>C | Probe | FAM | A | CGCGCCGAGGTGTAGGATCATGAGCAGGV (SEQ ID NO:374) |
| CYP2D6 H324P | 2935A>C | Probe | RED | C | ACGGACGCGGAGGGTAGGATCATGAGCAGV (SEQ ID NO:375) |
| CYP2D6 H324P | 2935A>C | Target | FAM | A | GCCTCCTGCTCATGATCCTACATCCGGATGTGCAGCGTGAGCCCAT (SEQ ID NO:376) |
| CYP2D6 H324P | 2935A>C | Target | RED | C | GCCTCCTGCTCATGATCCTACCTCCGGATGTGCAGCGTGAGCCCAT (SEQ ID NO:377) |
| | | | | | |
| CYP2D6 P34S | 100C>T | Invader | NONE | | GCAGTGGCAGGGGGCCTGGTGT (SEQ ID NO:378) |
| CYP2D6 P34S | 100C>T | Probe | RED | C | ACGGACGCGGAGGGTAGCGTGCAGCV (SEQ ID NO:379) |
| CYP2D6 P34S | 100C>T | Probe | FAM | T | CGCGCCGAGGAGTAGCGTGCAGCCV (SEQ ID NO:380) |
| CYP2D6 P34S | 100C>T | Target | RED | C | GCTGGGCTGCACGCTACCCACCAGGCCCCCTGCCACTGCCC (SEQ ID NO:381) |
| CYP2D6 P34S | 100C>T | Target | FAM | T | GCTGGGCTGCACGCTACTCACCAGGCCCCCTGCCACTGCCC (SEQ ID NO:382) |
| | | | | | |
| CYP2D6 883G>C | 883G>C | Invader | NONE | | AGGCCCTGACCCTCCCTCTGCAT (SEQ ID NO:383) |
| CYP2D6 883G>C | 883G>C | Probe | FAM | G | CGCGCCGAGGGTTGCGGCGCCV (SEQ ID NO:384) |
| CYP2D6 883G>C | 883G>C | Probe | RED | C | ACGGACGCGGAGCTTGCGGCGCCV (SEQ ID NO:385) |
| CYP2D6 883G>C | 883G>C | Target | FAM | G | AAGCGGCGCCGCAACTGCAGAGGGAGGGTCAGGGCCTCT (SEQ ID NO:386) |
| CYP2D6 883G>C | 883G>C | Target | RED | C | AAGCGGCGCCGCAAGTGCAGAGGGAGGGTCAGGGCCTCT (SEQ ID NO:387) |
| | | | | | |
| CYP2D6 1661G>C | 1661G>C | Invader | NONE | | GCGAGCAGAGGCGCTTCTCCGTT (SEQ ID NO:388) |
| CYP2D6 1661G>C | 1661G>C | Probe | FAM | G | CGCGCCGAGGGTCCACCTTGCGCV (SEQ ID NO:389) |
| CYP2D6 1661G>C | 1661G>C | Probe | RED | C | ACGGACGCGGAGCTCCACCTTGCGCV (SEQ ID NO:390) |
| CYP2D6 1661G>C | 1661G>C | Target | FAM | G | AGTTGCGCAAGGTGGACACGGAGAAGCGCCTCTGCTCGCGC (SEQ ID NO:391) |
| CYP2D6 1661G>C | 1661G>C | Target | RED | C | AGTTGCGCAAGGTGGAGACGGAGAAGCGCCTCTGCTCGCGC (SEQ ID NO:392) |
| | | | | | |
| CYP2D6 L421P | 3887T>C | Invader | NONE | | GCTTCACAAAGTGGCCCTGGGCATCCT (SEQ ID NO:393) |
| CYP2D6 L421P | 3887T>C | Probe | FAM | T | CGCGCCGAGGAGGAAGTGTTCGGGGV (SEQ ID NO:394) |
| CYP2D6 L421P | 3887T>C | Probe | RED | C | ACGGACGCGGAGGGGAAGTGTTCGGGV (SEQ ID NO:395) |
| CYP2D6 L421P | 3887T>C | Target | FAM | T | TCCACCCCGAACACTTCCTGGATGCCCAGGGCCACTTTGTGAAGCCG (SEQ ID NO:396) |
| CYP2D6 L421P | 3887T>C | Target | RED | C | TCCACCCCGAACACTTCCCGGATGCCCAGGGCCACTTTGTGAAGCCG (SEQ ID NO:397) |
| | | | | | |
| CYP2D6 T107I | 1023C>T | Invader | NONE | | CGCCCGCCTGTGCCCATCAA (SEQ ID NO:398) |
| CYP2D6 T107I | 1023C>T | Probe | FAM | C | CGCGCCGAGGCCCAGATCCTGGGTTV (SEQ ID NO:399) |
| CYP2D6 T107I | 1023C>T | Probe | RED | T | ACGGACGCGGAGTCCAGATCCTGGGTTTYV (SEQ ID NO:400) |
| CYP2D6 T107I | 1023C>T | Target | FAM | C | GCCCRAAACCCAGGATCTGGGTGATGGGCACAGGCGGGCGGT (SEQ ID NO:401) |
| CYP2D6 T107I | 1023C>T | Target | RED | T | GCCCRAAACCCAGGATCTGGATGATGGGCACAGGCGGGCGGT (SEQ ID NO:402) |
| | | | | | |
| CYP2D6 1973[Gins] | 1973[insG] | Invader | NONE | | CAGGCTGCTGGACCTAGCTCAGGAGGT (SEQ ID NO:403) |
| CYP2D6 1973[Gins] | 1973[insG] | Probe | RED | INS | acggacgcggagGGATCGAAGGAGGAGT (SEQ ID NO:404) |
| CYP2D6 1973[Gins] | 1973[insG] | Probe | FAM | DEL | CGCGCCGAGGGACTGAAGGAGGAGTCGV (SEQ ID NO:405) |
| CYP2D6 1973[Gins] | 1973[insG] | Target | RED | INS | CCCGACTCCTCCTTCGATCCCCTCCTGAGCTAGGTCCAGCAGCCTGAGT (SEQ ID NO:406) |
| CYP2D6 1973[Gins] | 1973[insG] | Target | FAM | DEL | AGCCCGACTCCTCCTTCAGTCCCTCCTGAGCTAGGTCCAGCAGCCTGAG (SEQ ID NO:407) |
| | | | | | |
| CYP2D6 3259insGT | 3259insGT | Invader | NONE | | GCCCTACACCACTGCCGTGATTCATGAGGC (SEQ ID NO:408) |
| CYP2D6 3259insGT | 3259insGT | Probe | FAM | INS | CGCGCCGAGGTGTGCAGCGCTTTGV (SEQ ID NO:409) |
| CYP2D6 3259insGT | 3259insGT | Probe | RED | DEL | ACGGACGCGGAGTGCAGCGCTTTGGV (SEQ ID NO:410) |

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FIGURE 15

| SNP Name | Nucleotide position/ change | Oligo Type | Dye | Poly-morphism | Assay Oligo Sequence |
|---|---|---|---|---|---|
| CYP2D6_3259insGT | 3259insGT | Target | FAM | INS | TGTCCCCAAAGCGCTGCACACCTCATGAATCACGGCAGTGGTGTAGGGCAT (SEQ ID NO:411) |
| CYP2D6_3259insGT | 3259insGT | Target | RED | DEL | TGTCCCCAAAGCGCTGCACCTCATGAATCACGGCAGTGGTGTAGGGCAT (SEQ ID NO:412) |
| | | | | | |
| CYP2D6_E410K | 3853G>A | Invader | NONE | | CATCRGTGCTGAAGGATGAGGCCGTCTGGT (SEQ ID NO:413) |
| CYP2D6_E410K | 3853G>A | Probe | RED | G | ACGGACGCGGAGGAGAAGCCCTTCCGV (SEQ ID NO:414) |
| CYP2D6_E410K | 3853G>A | Probe | FAM | A | CGCGCCGAGGAAGAAGCCCTTCCGCV (SEQ ID NO:415) |
| CYP2D6_E410K | 3853G>A | Target | RED | G | GGAAGCGGAAGGGCTTCTCCCAGACGGCCTCATCCTTCAGCACYGATGAC (SEQ ID NO:416) |
| CYP2D6_E410K | 3853G>A | Target | FAM | A | GGAAGCGGAAGGGCTTCTTCCAGACGGCCTCATCCTTCAGCACYGATGAC (SEQ ID NO:417) |
| | | | | | |
| CYP2D6_G42R | 124G>A | Invader | NONE | | GGCCCCCTGCCACTGCCCT (SEQ ID NO:418) |
| CYP2D6_G42R | 124G>A | Probe | RED | G | ACGGACGCGGAGGGGCTGGGCAACV (SEQ ID NO:419) |
| CYP2D6_G42R | 124G>A | Probe | FAM | A | CGCGCCGAGGAGGCTGGGCAACCV (SEQ ID NO:420) |
| CYP2D6_G42R | 124G>A | Target | RED | G | AGCAGGTTGCCCAGCCCGGGCAGTGGCAGGGGGCCTG (SEQ ID NO:421) |
| CYP2D6_G42R | 124G>A | Target | FAM | A | AGCAGGTTGCCCAGCCTGGGCAGTGGCAGGGGGCCTG (SEQ ID NO:422) |
| | | | | | |
| CYP2D6_R201H | 1943G>A | Invader | NONE | | CGCCGCTTCGAGTACGACGACCCTCT (SEQ ID NO:423) |
| CYP2D6_R201H | 1943G>A | Probe | FAM | G | CGCGCCGAGGGCTTCCTCAGGCTGV (SEQ ID NO:424) |
| CYP2D6_R201H | 1943G>A | Probe | RED | A | ACGGACGCGGAGACTTCCTCAGGCTGCV (SEQ ID NO:425) |
| CYP2D6_R201H | 1943G>A | Target | FAM | G | TCCAGCAGCCTGAGGAAGCGAGGGTCGTCGTACTCGAAGCGGCGCC (SEQ ID NO:426) |
| CYP2D6_R201H | 1943G>A | Target | RED | A | TCCAGCAGCCTGAGGAAGTGAGGGTCGTCGTACTCGAAGCGGCGCC (SEQ ID NO:427) |
| | | | | | |
| CYP2D6_R440H | 4042G>A | Invader | NONE | | CCCTCCCCTCCCCACAGGCCT (SEQ ID NO:428) |
| CYP2D6_R440H | 4042G>A | Probe | FAM | G | CGCGCCGAGGGCCGTGCATGCCV (SEQ ID NO:429) |
| CYP2D6_R440H | 4042G>A | Probe | RED | A | ACGGACGCGGAGACCGTGCATGCCTV (SEQ ID NO:430) |
| CYP2D6_R440H | 4042G>A | Target | FAM | G | CCCGAGGCATGCACGGCGGCCTGTGGGGAGGGGAGGGGC (SEQ ID NO:431) |
| CYP2D6_R440H | 4042G>A | Target | RED | A | CCCGAGGCATGCACGGTGGCCTGTGGGGAGGGGAGGGGC (SEQ ID NO:432) |
| | | | | | |
| CYP2D6_V11M | 31G>A | Invader | NONE | | AGAAGCACTGGTGCCCCTGGCCT (SEQ ID NO:433) |
| CYP2D6_V11M | 31G>A | Probe | FAM | G | CGCGCCGAGGGTGATAGTGGCCATCTTCV (SEQ ID NO:434) |
| CYP2D6_V11M | 31G>A | Probe | RED | A | ACGGACGCGGAGATGATAGTGGCCATCTTCV (SEQ ID NO:435) |
| CYP2D6_V11M | 31G>A | Target | FAM | G | GCAGGAAGATGGCCACTATCACGGCCAGGGGCACCAGTGCTTCTAG (SEQ ID NO:436) |
| CYP2D6_V11M | 31G>A | Target | RED | A | GCAGGAAGATGGCCACTATCATGGCCAGGGGCACCAGTGCTTCTAG (SEQ ID NO:437) |
| | | | | | |
| CYP2D6_V338M | 3183G>A | Invader | NONE | | GGCCGTGTCCAACAGGAGATCGACGACT (SEQ ID NO:438) |
| CYP2D6_V338M | 3183G>A | Probe | RED | G | ACGGACGCGGAGGTGATAGGGCAGGTGV (SEQ ID NO:439) |
| CYP2D6_V338M | 3183G>A | Probe | FAM | A | CGCGCCGAGGATGATAGGGCAGGTGCV (SEQ ID NO:440) |
| CYP2D6_V338M | 3183G>A | Target | RED | G | CGCCGCACCTGCCCTATCACGTCGTCGATCTCCTGTTGGACACGGCCTG (SEQ ID NO:441) |
| CYP2D6_V338M | 3183G>A | Target | FAM | A | CGCCGCACCTGCCCTATCATGTCGTCGATCTCCTGTTGGACACGGCCTG (SEQ ID NO:442) |
| | | | | | |
| CYP2D6_V7M | 19G>A | Invader | NONE | | TGGCCACTATCAYGGCCAGGGGCAA (SEQ ID NO:443) |
| CYP2D6_V7M | 19G>A | Probe | RED | G | ACGGACGCGGAGCCAGTGCTTCTAGCCV (SEQ ID NO:444) |
| CYP2D6_V7M | 19G>A | Probe | FAM | A | CGCGCCGAGGTCAGTGCTTCTAGCCCV (SEQ ID NO:445) |
| CYP2D6_V7M | 19G>A | Target | RED | G | TATGGGGCTAGAAGCACTGGTGCCCCTGGCCRTGATAGTGGCCATC (SEQ ID NO:446) |
| CYP2D6_V7M | 19G>A | Target | FAM | A | TATGGGGCTAGAAGCACTGATGCCCCTGGCCRTGATAGTGGCCATC (SEQ ID NO:447) |
| | | | | | |
| CYP2D6_2549A>del | | Invader | NONE | | GCTGGGCTGGGTCCCAGGTCATCT (SEQ ID NO:448) |
| CYP2D6_2549A>del | | Probe | RED | INS | ACGGACGCGGAGCTGTGCTCAGTTAGCAGV (SEQ ID NO:449) |
| CYP2D6_2549A>del | | Probe | FAM | DEL | CGCGCCGAGGCGTGCTCAGTTAGCAGV (SEQ ID NO:450) |
| CYP2D6_2549A>del | | Target | RED | INS | ATGAGCTGCTAACTGAGCACAGGATGACCTGGGACCCAGCCCAGCCC (SEQ ID NO:451) |
| CYP2D6_2549A>del | | Target | FAM | DEL | ATGAGCTGCTAACTGAGCACGGATGACCTGGGACCCAGCCCAGCCC (SEQ ID NO:452) |
| | | | | | |
| CYP2D6_1707T>del | | Invader | NONE | | CAGGCGGCCTCCTCGGTCACCT (SEQ ID NO:453) |
| CYP2D6_1707T>del | | Probe | FAM | INS | CGCGCCGAGGCACTGCTCCAGCGAV (SEQ ID NO:454) |
| CYP2D6_1707T>del | | Probe | RED | DEL | ACGGACGCGGAGCCTGCTCCAGCGACV (SEQ ID NO:455) |
| CYP2D6_1707T>del | | Target | FAM | INS | AGAAGTCGCTGGAGCAGTGGGTGACCGAGGAGGCCGCCTGCC (SEQ ID NO:456) |
| CYP2D6_1707T>del | | Target | RED | DEL | AGAAGTCGCTGGAGCAGGGGTGACCGAGGAGGCCGCCTGCC (SEQ ID NO:457) |
| | | | | | |

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FIGURE 15

| SNP Name | Nucleotide position/ change | Oligo Type | Dye | Poly-morphism | Assay Oligo Sequence |
|---|---|---|---|---|---|
| CYP2D6 1039C>T V3 | 1039C>T | Invader | NONE | | CTTGCCTTGGGAACGCGGCCCT (SEQ ID NO:458) |
| CYP2D6 1039C>T V3 | 1039C>T | Probe | FAM | C | CGCGCCGAGGGAAACCCAGGATCTGGGV (SEQ ID NO:459) |
| CYP2D6 1039C>T V3 | 1039C>T | Probe | RED | T | ACGGACGCGGAGAAAACCCAGGATCTGGGV (SEQ ID NO:460) |
| CYP2D6 1039C>T V3 | 1039C>T | Target | FAM | C | TCACCCAGATCCTGGGTTTCGGGCCGCGTTCCCAAGGCAAGCA (SEQ ID NO:461) |
| CYP2D6 1039C>T V3 | 1039C>T | Target | RED | T | TCACCCAGATCCTGGGTTTTGGGCCGCGTTCCCAAGGCAAGCA (SEQ ID NO:462) |
| | | | | | |
| CYP2D6 R296C V4 | 2850C>T | Invader | NONE | | GGCAGAGAACAGGTCAGCCACCACTATGCT (SEQ ID NO:463) |
| CYP2D6 R296C V4 | 2850C>T | Probe | RED | C | ACGGACGCGGAGGCAGGTTCTCATCATTGAAGV (SEQ ID NO:464) |
| CYP2D6 R296C V4 | 2850C>T | Probe | FAM | T | CGCGCCGAGGACAGGTTCTCATCATTGAAGCV (SEQ ID NO:465) |
| CYP2D6 R296C V4 | 2850C>T | Target | RED | C | GCAGCTTCAATGATGAGAACCTGCGCATAGTGGTGGCTGACCTGTTCTCTGCCGG (SEQ ID NO:466) |
| CYP2D6 R296C V4 | 2850C>T | Target | FAM | T | GCAGCTTCAATGATGAGAACCTGTGCATAGTGGTGGCTGACCTGTTCTCTGCCGG (SEQ ID NO:467) |
| | | | | | |
| CYP2D6*8 G169X 1/3 | 1758G>T | Invader | NONE | | TGTGCCGCCTTCGCCRACCACTCyC (SEQ ID NO:468) |
| CYP2D6*8 G169X 1/3 | 1758G>T | Probe | FAM | G | CGCGCCGAGGGGTGGGTGATGGGCV (SEQ ID NO:469) |
| CYP2D6*8 G169X 1/3 | 1758G>T | Probe | RED | T | ACGGACGCGGAGTGTGGGTGATGGGCV (SEQ ID NO:470) |
| CYP2D6*8 G169X 1/3 | 1758G>T | Target | FAM | G | TTCTGCCCATCACCCACCrGAGTGGTYGGCGAAGGCGGCACAAA (SEQ ID NO:471) |
| CYP2D6*8 G169X 1/3 | 1758G>T | Target | RED | T | TTCTGCCCATCACCCACArGAGTGGTYGGCGAAGGCGGCACAAA (SEQ ID NO:472) |
| | | | | | |
| CYP2D6*14 G169R 1/3 | 1758G>A | Invader | NONE | | TGTGCCGCCTTCGCCRACCACTCyT (SEQ ID NO:473) |
| CYP2D6*14 G169R 1/3 | 1758G>A | Probe | FAM | G | CGCGCCGAGGGGTGGGTGATGGGCV (SEQ ID NO:474) |
| CYP2D6*14 G169R 1/3 | 1758G>A | Probe | RED | A | ACGGACGCGGAGAGTGGGTGATGGGCV (SEQ ID NO:475) |
| CYP2D6*14 G169R 1/3 | 1758G>A | Target | FAM | G | TTCTGCCCATCACCCACCrGAGTGGTYGGCGAAGGCGGCACAAA (SEQ ID NO:476) |
| CYP2D6*14 G169R 1/3 | 1758G>A | Target | RED | A | TTCTGCCCATCACCCACTrGAGTGGTYGGCGAAGGCGGCACAAA (SEQ ID NO:477) |
| | | | | | |
| CYP2D6 H94R AS | 984A>G | Invader | NONE | | TGCGCGAGGCGMTGGTGACCCT (SEQ ID NO:478) |
| CYP2D6 H94R AS | 984A>G | Probe | FAM | A | CGCGCCGAGGACGGCGAGGACACcV (SEQ ID NO:479) |
| CYP2D6 H94R AS | 984A>G | Probe | RED | G | ACGGACGCGGAGGCGGCGAGGACACV (SEQ ID NO:480) |
| CYP2D6 H94R AS | 984A>G | Target | FAM | A | TCGGCSGTGTCCTCGCCGTGGGTCACCAKCGCCTCGCGCACG (SEQ ID NO:481) |
| CYP2D6 H94R AS | 984A>G | Target | RED | G | TCGGCSGTGTCCTCGCCGCGGGTCACCAKCGCCTCGCGCACG (SEQ ID NO:482) |
| | | | | | |
| CYP2D6 2539-2542[delAACT] | 2539-2542[delAACT] | Invader | NONE | | GCTGGGTCCCAGGTCATCCGTGCTT (SEQ ID NO:483) |
| CYP2D6 2539-2542[delAACT] | 2539-2542[delAACT] | Invader | NONE | | GCTGGGTCCCAGGTCATCCTGTGCTT (SEQ ID NO:484) |
| CYP2D6 2539-2542[delAACT] | 2539-2542[delAACT] | Probe | FAM | DEL | cgcgccgaggCAGCAGCTCATCCAG (SEQ ID NO:485) |
| CYP2D6 2539-2542[delAACT] | 2539-2542[delAACT] | Probe | RED | INS | acggacgcggagCAGTTAGCAGCTCATCC (SEQ ID NO:486) |
| CYP2D6 2539-2542[delAACT] | 2539-2542[delAACT] | Target | FAM | DEL | ACCCAGCTGGATGAGCTGCTGAGCACGGATGACCTGGGACCCAGCCC (SEQ ID NO:487) |
| CYP2D6 2539-2542[delAACT] | 2539-2542[delAACT] | Target | FAM | DEL | ACCCAGCTGGATGAGCTGCTGAGCACAGGATGACCTGGGACCCAGCCC (SEQ ID NO:488) |
| CYP2D6 2539-2542[delAACT] | 2539-2542[delAACT] | Target | RED | INS | ACCCAGCTGGATGAGCTGCTaactgAGCACGGATGACCTGGGACCCAGCCC (SEQ ID NO:489) |
| CYP2D6 2539-2542[delAACT] | 2539-2542[delAACT] | Target | RED | INS | ACCCAGCTGGATGAGCTGCTaactgAGCACAGGATGACCTGGGACCCAGCCC (SEQ ID NO:490) |
| | | | | | |
| CYP2D6 2613-2615delAGA | 2613-2615delAGA | Invader | NONE | | CCACCGTGGCAGCCACTCTCACCC (SEQ ID NO:491) |
| CYP2D6 2613-2615delAGA | 2613-2615delAGA | Probe | FAM | INS | CGCGCCGAGGTTCTCCATCTCTGCCAV (SEQ ID NO:492) |
| CYP2D6 2613-2615delAGA | 2613-2615delAGA | Probe | RED | DEL | ACGGACGCGGAGTCCATCTCTGCCAGGV (SEQ ID NO:493) |
| CYP2D6 2613-2615delAGA | 2613-2615delAGA | Target | FAM | INS | GCCTTCCTGGCAGAGATGGAGAAGGTGAGAGTGGCTGCCACGGTGGGG (SEQ ID NO:494) |
| CYP2D6 2613-2615delAGA | 2613-2615delAGA | Target | RED | DEL | GCCTTCCTGGCAGAGATGGAGGTGAGAGTGGCTGCCACGGTGGGG (SEQ ID NO:495) |
| | | | | | |
| CYP2D6 172-174FRPrep(a) is | ]2 | Invader | NONE | | CCCCARGACGCCCCTTTCGCCCT (SEQ ID NO:496) |
| CYP2D6 172-174FRPrep(a) is | ]2 | Probe | FAM | INS | CGCGCCGAGGCTTTCGCCCCTTTCGV (SEQ ID NO:497) |
| CYP2D6 172-174FRPrep(a) is | ]2 | Probe | RED | DEL | ACGGACGCGGAGCAACGGTCTCTTGGACV (SEQ ID NO:498) |
| CYP2D6 172-174FRPrep(a) is | ]2 | Target | FAM | INS | CTTTGTCCAAGAGACCGTTGGGGCGAAAGGGGCGAAAGGGGCGAAAGGGGCGTCYTGGGGGT (SEQ ID NO:499) |
| CYP2D6 172-174FRPrep(a) is | ]2 | Target | RED | DEL | CTTTGTCCAAGAGACCGTTGGGGCGAAAGGGGCGTCYTGGGGGT (SEQ ID NO:500) |
| | | | | | |
| CYP2D6 221C>A as | | Invader | NONE | | GGAGGGCGGCAGAGGTSCTGAGGT (SEQ ID NO:501) |
| CYP2D6 221C>A as | | Probe | RED | C | ACGGACGCGGAGCTcCCCtACCAGAAGCAV (SEQ ID NO:502) |
| CYP2D6 221C>A as | | Probe | FAM | A | CGCGCCGAGGATgCCCcACCAGAAV (SEQ ID NO:503) |
| CYP2D6 221C>A as | | Target | RED | C | ATGTTTGCTTCTGGTaGGGgAGCCTCAGSACCTCTGCCGCCCTCCAG (SEQ ID NO:504) |
| CYP2D6 221C>A as | | Target | FAM | A | ATGTTTGCTTCTGGTgGGGcATCCTCAGSACCTCTGCCGCCCTCCAG (SEQ ID NO:505) |
| | | | | | |

"Replacement Sheet"

FIGURE 15

| SNP Name | Nucleotide position/ change | Oligo Type | Dye | Poly-morphism | Assay Oligo Sequence |
|---|---|---|---|---|---|
| CYP2D6 221C>A s | | Invader | NONE | | CCCACCATCCATGTTTGCTTCTGGTRGGGSAC (SEQ ID NO:506) |
| CYP2D6 221C>A s | | Probe | FAM | C | CGCGCCGAGGGCCTCAGcACCTCTGV (SEQ ID NO:507) |
| CYP2D6 221C>A s | | Probe | RED | A | ACGGACGCGGAGTCCTCAGgACCTCTGCV (SEQ ID NO:508) |
| CYP2D6 221C>A s | | Target | FAM | C | GGCGGCAGAGGTgCTGAGGCTSCCCYACCAGAAGCAAACATGGATGGTGGGTG (SEQ ID NO:509) |
| CYP2D6 221C>A s | | Target | RED | A | GGCGGCAGAGGTcCTGAGGATSCCCYACCAGAAGCAAACATGGATGGTGGGTG (SEQ ID NO:510) |
| | | | | | |
| CYP2D6 223C>G as | | Invader | NONE | | GGAGGGCGGCAGAGGTSCTGAGGMTT (SEQ ID NO:511) |
| CYP2D6 223C>G as | | Probe | RED | C | ACGGACGCGGAGCCCCtACCAGAAGCAAacV (SEQ ID NO:512) |
| CYP2D6 223C>G as | | Probe | FAM | G | CGCGCCGAGGGCCCcACCAGAAGCV (SEQ ID NO:513) |
| CYP2D6 223C>G as | | Target | RED | C | ATGTTTGCTTCTGGTaGGGGAgCCTCAGcACCTCTGCCGCCCTCCAG (SEQ ID NO:514) |
| CYP2D6 223C>G as | | Target | FAM | G | ATGTTTGCTTCTGGTgGGGCAaCCTCAGgACCTCTGCCGCCCTCCAG (SEQ ID NO:515) |
| | | | | | |
| CYP2D6 223C>G s | | Invader (mutant) | NONE | | CCACCCATGTTTGCTGGTGGTGGGGT (SEQ ID NO:516) |
| CYP2D6 223C>G s | | Invader (wild-type) | NONE | | ACCCACCATCCATGTTTGCTTCTGGTRGGGT (SEQ ID NO:517) |
| CYP2D6 223C>G s | | Probe | RED | C | ACGGACGCGGAGGAgCCTCAGcACCTCV (SEQ ID NO:518) |
| CYP2D6 223C>G s | | Probe | FAM | G | CGCGCCGAGGCAtCCTCAGgACCTCTGV (SEQ ID NO:519) |
| CYP2D6 223C>G s | | Target | RED | C | GGCGGCAGAGGTgCTGAGGcTCCCCtACCAGAAGCAAACATGGATGGTGGGTGA (SEQ ID NO:520) |
| CYP2D6 223C>G s | | Target | FAM | G | GGCGGCAGAGGTcCTGAGGaTGCCCcACCAGAAGCAAACATGGATGGTGGGTGA (SEQ ID NO:521) |
| | | | | | |
| Copy Number Designs | Gene | Oligo | Sequence | | |
| E | 2D6 | 2D6 Invader | CCCGCGCCACCCACACTGAGCC (SEQ ID NO:522) | | |
| E | Alpha Actin | Alpha Actin Invader | AGGAGTAGCCACGCTCGGTGAGGATCTTCATT (SEQ ID NO:523) | | |
| E | 2D6 | Probe Arm3 2D6 | ACGGACGCGGAGTTACAGCACAGGTGC (SEQ ID NO:524) | | |
| E | Alpha Actin | Probe Arm1 Alpha Actin | CGCGCCGAGGCAGGTAGTCGGTGAGATC (SEQ ID NO:525) | | |
| E | 2D6 | Synthetic Target Alpha Ac | GGACCGCACCTGTGCTGTAaGCTCAGTGTGGGTGGCGCGGGGC (SEQ ID NO:526) | | |
| E | Alpha Actin | Synthetic Target 2D6 | CGCGATCTCACCGACTACCTGAATGAAGATCCTCACCGAGCGTGGCTACTCCTTC (SEQ ID NO:527) | | |

FRET SEQUENCES
SEQ ID 242 (FRET probe FAM): Y-tct-X-agc-cgg-ttt-tcc-ggc-tga-gac-ctc-ggc-gcg-hex

SEQ ID 243 (FRET probe RED): Y-tct-X-agc-cgg-ttt-tcc-ggc-tga-gac-tcc-gcg-tcc-gt-hex

"Replacement Sheet"